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OM protein - protein search, using sw model

Run on: July 6, 2006, 01:28:04 ; Search time 316 Seconds
(without alignments)
3061.919 Million cell updates/sec

Title: US-10-771-931-1
Perfect score: 5357
Sequence: 1 MTNCKYKRLKSLVGLVSVGT.....PTIIGAAGLSKGRDTEGN 1046

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5357	100.0	1046	2	084941_STRPY
2	3575.5	66.7	1027	2	093T51_STRPY
3	3501	65.4	1026	2	048R34_STRPM
4	3442.5	63.9	1023	2	093T53_STRPY
5	3371.5	62.9	1025	2	054507_STRPY
6	3370	62.9	1026	2	09X3R6_STRPY
7	3357.5	62.7	1025	2	P72532_STRPY
8	3164.5	59.1	1013	2	091953_STRPY
9	3132.5	58.5	1015	2	093T50_STRPY
10	2973.5	55.5	1013	2	093T52_STRPY
11	2878.5	53.7	954	2	06YB06_STRPY
12	2834	52.9	1022	2	093T54_STRPY
13	2779.5	51.9	963	2	093T49_STRPY
14	2654.5	49.6	1029	2	09X242_STRPY
15	2571	48.0	862	2	09R222_STRPY
16	2531	47.2	923	2	09S432_STRPY
17	2488	46.4	865	2	09S439_STRPY
18	2465	46.0	873	2	09S430_STRPY
19	2460.5	45.9	872	2	09S443_STRPY
20	2439.5	45.5	854	2	09S338_STRPY
21	2329	43.5	861	2	09R074_STRPY
22	2138.5	39.9	1091	2	006556_STRPY
23	2102	37.2	746	2	08V595_STRPY
24	1458.5	29.2	409	2	09X999_STRPY
25	1391.5	26.0	456	2	09XCK8_STRPY
26	1388.5	25.9	471	2	09R228_STRPY
27	1376.5	25.7	447	2	09R007_STRPY
28	1343	25.1	452	2	09XCK2_STRPY
29	1331.5	24.9	439	2	09R008_STRPY
30	1276	23.8	454	2	09S418_STRPY
31	1262	23.6	423	2	09R226_STRPY

32	1247.5	23.3	435	2	09X9C0_STRPY	09X9C0 streptococc
33	1238.5	23.1	437	2	09R227_STRPY	09R227 streptococc
34	1231.5	23.0	441	2	09R229_STRPY	09R229 streptococc
35	1229	22.9	410	2	09R229_STRPY	09R229 streptococc
36	1219	22.8	253	2	09R492_STRPY	09R492 streptococc
37	1191	22.2	434	2	09R6H2_STRPY	09R6H2 streptococc
38	1190.5	22.2	430	2	09X613_STRPY	09X613 streptococc
39	1093.5	20.4	938	2	03ZJF8_STRSU	03ZJF8 streptococc
40	1064	19.9	421	2	09R225_STRPY	09R225 streptococc
41	1025.5	19.1	383	2	09L5D7_STRPY	09L5D7 streptococc
42	845.5	15.8	564	2	0300K5_STRSU	0300K5 streptococc
43	806.5	15.1	261	2	09R475_STRPY	09R475 streptococc
44	774.5	14.5	258	2	09X6H5_STRPY	09X6H5 streptococc
45	708.5	13.2	250	2	09X6H0_STRPY	09X6H0 streptococc

ALIGNMENTS

RESULT 1
084941_STRPY PRELIMINARY; PRT; 1046 AA.
ID 084941_STRPY
AC 084941;
DT 01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1998, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Serum opacity factor.
GN Name=sof2;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=1314;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T2MR;
RX MEDLINE=9232508; PubMed=10216862;
RA Courtney H.S., Hasty D.L., Li Y., Chiang H.C., Thacker J.L.,
RA Dale U.B.;
RT "Serum opacity factor is a major fibronectin-binding protein and a
RT virulence determinant of M type 2 Streptococcus pyogenes.";
RL Mol. Microbiol. 32:89-98(1999).
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC EMBL; AF019890; AAC32596.1; -; Genomic DNA.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009975; C:cell wall (sensus Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fibron repeat_bd.
DR InterPro; IPR005877; Gpos YSIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR002035; VMP_A.
DR Pfam; PF02986; Fn_bind; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF00092; VMA; 1.
DR SMART; SM00327; VMA; 1.
DR TIGRfam; TIGR01168; YSIRK signal; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS00234; VMP_A; 1.
DR SQUONCE; 1046 AA; 114914 MW; B12CF6B68059B62 CRC64;
Query Match 100.0%; Score 5357; DB 2; Length 1046;
Best Local Similarity 100.0%; Pred. No. 3.1e-205;
Matches 1046; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTNCKYKRLKSLVGLVSVGTMLIAPVLAQVSASTSTSTSTASAGVTSSTASETGS 60
DB 1 MTNCKYKRLKSLVGLVSVGTMLIAPVLAQVSASTSTSTSTASAGVTSSTASETGS 60
QY 61 GAATTAATTTATNGPGSTPAVNAATPOQALAPVAATASTSSASSSGKAPQAVT 120

07-FEB-2006, entry version 16.
 Serum opacity factor v721.
 Streptococcus pyogenes.
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.
 NCBI_Taxid=1314;
 [1]
 NUCLEOTIDE SEQUENCE.
 MEDLINE=21642587; PubMed=11782509;
 RA Gillen C.M., Towers R.J., McMillan D.J., Delvecchio A.,
 RA Sriperaksh K.S., Currie B., Kreitemeyer B., Chhatwal G.S.,
 RA Walker M.J.;
 RT "Immunological response mounted by Aboriginal Australians living in
 RT the Northern Territory of Australia against Streptococcus pyogenes
 RT serum opacity factor.";
 RL Microbiology 148:169-178 (2002).
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 CC EMBL, AF367014; AK52968.1; -; Genomic DNA.
 DR GO; GO:0009986; C:cell surface; IEA.
 DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR004237; Fibron repeat_bd.
 DR InterPro; IPR005877; Gpos_YSTRK.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF02986; Fn_bnd; 3.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF00092; VWA; 1.
 DR SPKAT; SM00327; VWA; 1.
 DR TIGRFAMs; TIGR01168; YSTRK_signal; 1.
 DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
 DR PROSITE; PS50234; VWFA; 1.
 DR SEQUENCE 1027 AA; 112542 MW; 048239E8598AC7A CRC64;

 Query Match 66.7%; Score 3575.5; DB 2; Length 1027;
 Best Local Similarity 70.1%; Pred. No. 2.8e-134;
 Matches 751; Conservative 98; Mismatches 153; Indels 69; Gaps 26;

 QY 1 MTNCKYKARKLVGLVGVNGLIAPTVLQVSVAST--TSTETSTASAGVSGTASAE 57
 Db 1 MTNCKYKARKLVSVLNVGVNGLIAPTVLQVGVNTANTETSTPATTPAGGTGA----- 54
 QY 58 TGSAAVTTATTTT-----ATTNGGPOSTPVAEAETPOPAQIAEVAAT 102
 Db 55 TTSGTATTTTSATTTDAGGAGSGTNGASVTVSSGSGSOS -GTTPASPGQAQTTP -AAT 111
 QY 103 STSSASSSDGKAPQAVTSSSTSPSTPAASNGSNGQASASATPEPTMVEKKTVDKENS 162
 Db 112 SIS-SNSSSGQILPK--TALTSPSTPAASNN-SNOEASATETPOTMVEKKTVDKEN-Q 166
 QY 163 LNIIDGTPKTKGSSVNNKPTKLRNPDGKLRDIVDVYTRTKYTNEDGTLDTVYVTKPKOI 222
 Db 167 AKYDGGKPKKGGV-DKDKTKLRNPDGKLRDIVDVYTRTKYTNEDGTLDTVYVTKPKOI 225
 QY 223 DEGADVALLDVSKKMSDDFNNAKNKIKGLVTKLTLSKASNSDNDKHTKNSRNSVRLMT 282
 Db 226 DEGADVALLDVSKKMSDDFNNAKNKIKGLV-TLT--GTKNGGGRHK--ARNSVRLMT 279
 QY 283 FYRHSNPIDISGTEBOLDKLDDAKKAAKANDKMGVYDLOGAIIHKAEIFPKYKEKFG 342
 Db 280 FYRHSNPIDISGTEBOLDLTLNKKOEADKEDVWGVDYDGAIIHKAIDVNRKEKESK 339

DT 07-FEB-2006, entry version 16.
DE Serum opacity factor VT21.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=1314;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21642587; PubMed=11782509;
RA Gillen C.M., Towers R.J., McMillan D.J., Delvecchio A.,
RA Sripierakash K.S., Currie B., Kreklemeyer B., Chinatal G.S.,
RA Walker M.J.;
RT "Immunological response mounted by Aboriginal Australians living in
RT the Northern Territory of Australia against Streptococcus pyogenes
RT serum opacity factor".
RL Microbiology 148:169-178 (2002).
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DR EMBL; AF367014; AAK52968.1; -, Genomic DNA.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (sensu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Fibron repeat_Dc.
DR InterPro; IPR005877; Gpos_YsIRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF02986; Fn_bind; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF00092; VWA; 1.
DR SMART; SMO03327; VWA; 1.
DR TIGRFAMs; TIGR01168; YsIRK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS50234; VWEA_1.
SQ SEQUENCE 1027 AA; 112542 MW; 0482398558A4C7A CRC64;

Query Match	66.7%;	Score 3575.5;	DB 2;	Length 1027;
Best Local Similarity	70.1%;	Pred. No. 2.8e-134;		
Matches 751;	Conservative 98;	Mismatches 153;	Indels 69;	Gaps 26
QY	1	MTNCKYLRKRLSVGLSVGVMILNAPTVLVQSVAST--ISTETISASAGVIGTSGTAASE	57	
Db	1	MTNCKYLRKRLSVGLSVGVMILNAPTVLVQSVAST--ISTETISASAGVIGTSGTAASE	54	
QY	58	TGSGAATVTAATTT-----ATTNGGPSTPAVAAKTPPOPOAIAVAAT	102	
Db	58	TGSGAATVTAATTT-----ATTNGGPSTPAVAAKTPPOPOAIAVAAT	102	
QY	103	STSSASSSSDQKAPQAVTSTSPSTPAASNGSNGQEAETEPOTMVEVEKTVDKENS	162	
Db	112	SIS-SSSSDQKIR--TAITSPTPAASNN-SNGRMSATTEPOTMVEVEKTVDKEN-Q	166	
QY	163	LNIRKGTPTKGTSSVNNKQTKLRNRDQKLRDIVVTRYVTKNEDGTFIDVTVYVKQOI	222	
Db	167	AKYDQGKPKNGSSSV-DDKQTKLRNRDQKLRDIVVTRYVTKNEDGTFIDVTVYVKQOI	225	
QY	223	DEGADVALLDVSKMSSEDDPNNAKQTKKLVTKLTSSAASNDDEHKNSRNSVRLMT	282	
Db	226	DEGADVALLDVSKMSSEDDPNNAKQTKKLV-TLT--GQKNGGKHK--AENSVRLLMT	279	
QY	283	FYRRIISPIDISGKTBEQLDKLTDLKKKAKANDWGVLDGALAHKAEIFNKCEKKEFG	342	
Db	280	FYRRIKPIDISGKTBEQLDLTKNAQEAQDQVWGVLDGALAHKADVFNKKEKESK	339	
QY	343	KRRHIVLPQGESEFSTYELQNSVREDYTKYLRLSGAVTSSNPLLPWPIFNHTKNIIML	402	
Db	340	KRQHVIVPQGESEFSTYDIRN--KDKKQKQKTLTYTTTSSNPPLSFMPFIPIHTRKADMI	396	
QY	403	DDVNVNPKLGQTLGIAGLDNLQSTLSISTGSSLAGAFLLGGGSLTEYVTLLEKYSGLKE	462	
Db	397	DDIKTLIKQSAALGIBELGKDKLSSAGLASSALGGLFGQSGFLTEYVTLLEKYSQDSLSKA	456	

171 PKTSSVNNKEDTKLIRNBDKLDLDVDTYRTYKTNEDGTIDVTVYKPKQIDEGADVMA 230
 170 -----KAKQKIRBDBNDPKDLPDVRKVKDNDGDLDTLTKMPKQIDEGADVMA 221
 231 LLDVSKKMSDDPFNNANKIKGLVLTLSKASNSDNDKHKYNSRNSVRLMTFYREISNP 230
 222 LLDVSKKMSDDPFNNANKIKGLVLTLSKASNSDNDKHKYNSRNSVRLMTFYREISNP 227
 291 IDISGTEBOLDKLDLDRKAKANVWDVLOGAHKAEIRNKEKKEKFGKRRHVL 350
 278 TEL---TTKQVDAKKEVMDQAKKMDVMDVLOGAHKAEIRNKEKKEKFGKRRHVL 332
 351 SGGSTSTYSLQNSVREDTKLSTLSGAVTSSNPLPMPPIFNTHKNIMLDDVKNLVK 410
 333 SGGSTSTYSLQNSVREDTKLSTLSGAVTSSNPLPMPPIFNTHKNIMLDDVKNLVK 391
 411 LGOTLGIAGLDNOSTLSLSTGSSLAGAFGGSLTEYTLTKKYSGDLEKNOFDYTKR 470
 392 WGEGLGIBGLDNLNTLKTAGAASGIVGGFLGGSLTEYTLTKKYSGDLEKNOFDYTKR 451
 471 VGESEYHPSERKKTGEIRPKSEIEPKIKELFENNNKNDKSWTEWIFDKLSTETK 530
 452 VGESEYHPSERKKTGEIRPKSEIEPKIKELFENNNKNDKSWTEWIFDKLSTETK 506
 531 AKQETLMKLELYLTKKRYHYNNHLSAIAKAAQOEGTFYVVDVDTLTKTSKRVKQ 590
 507 AKESAILKLVLPYFKRDYIYNNHLSAIAKAAQOEGTFYVVDVDTLTKTSKRVKQ 566
 591 VESBEDKKKORHDEKRNKFPNNTLKQSEGGKDPFEDVDKAEKEDLTVNTYET 650
 567 VKSEBDKKKAEKKEIRKDEKEDNYSKMSSEKKEFPNDVDKAEKEDLTVNTYET 626
 651 PEDGVNKNQNSQVSSNNNSLHNSYKVTAKASDASWMSLY-SNKSLETLTSSKQK 709
 627 FGNVSVSSGSKMSLGSNSG--SSSRKYSKGRDSGLSLSTGSKSLTWLTSKQK 684
 710 BAFKNSSLTYKTKLQVKKQKLDKNNK-----TKDSTENKTSYTKOISLTVYK 763
 665 QAFEGKELTLYLKLKDKDKRETKKQOESRRIRKKAASSESNTVETLTSKISYK 744
 764 INN-QEVGNGLDDVGLTYTKEFVVPVVEGSEV--PIPEKPLVEMTPLYPAINYP 820
 745 INNGDTONNKLSEKVSYSKMPPIELDIEVVPVPEKPLVEMTPLYPAINYP 801
 821 DIPQLPREDLEISGHPGVVDIYEDTGTABGAGQNVSTOBNRDIYDITEDTOP 880
 802 --PTQLPREDLEISGHPGVVDIYEDTGTABGAGQNVSTOBNRDIYDITEDTOP 859
 881 GMSGNDATVVEEDTAPKRPDVLVGGQSPDITEDTOPSVGSDNATVVEEDTAPKRPD 940
 860 GMSGNDATVVEEDTAPKRPDVLVGGQSPDITEDTOPSVGSDNATVVEEDTAPKRPD 919
 941 SLVGGQSDIDITEDTOPGMSGNGATVIEBTPRPKVPFNPNPEQAPKPEKPEBLSLP 1000
 920 IIVGGQSDIDITEDTOPGMSGNDATVIEBTPRPKVPFNPNPEQAPKPEKPEBLSLP 979
 1001 QAPVYKAHLTPASGDKREASPTIAPTTIGAGLISKRRDTEGN 1046
 980 QAPVYKAHLTPASGDKREASPTIAPTTIGAGLISKRRDTEGN 1025

RESULT 2
 S33850
 fibronectin-binding protein - Streptococcus dysgalactiae
 C:Species: Streptococcus dysgalactiae
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S33850, S32632
 R:Binding: P.E.; McGavin, M.U.; Sigaard, C.; Guse, B.; Gursiddappa, S.; Hoesek, M.; Li
 Eur. J. Biochem. 214, 819-827, 1993
 A:Title: Two different genes coding for fibronectin-binding proteins from Streptococcus
 A:Reference number: S33850, MUID:93307299, PMID:8319691

Query Match 39.9%; Score 2138.5; DB 2; Length 1091;
 A:Residues: 1-1091 <LIN>
 A:Cross-references: UNIPROT:Q06556; UNIPARC:UPI00000B92C0; EMBL:Z22150; NID:9288966; PI
 Best Local Similarity 42.3%; Pred. No. 1.5e-80;
 Matches 487; Conservative 184; Mismatches 310; Indels 171; Gaps 28;

A:Molecule type: DNA
 A:Residues: 1-1091 <LIN>
 A:Cross-references: UNIPROT:Q06556; UNIPARC:UPI00000B92C0; EMBL:Z22150; NID:9288966; PI
 Query Match 39.9%; Score 2138.5; DB 2; Length 1091;
 A:Residues: 1-1091 <LIN>
 A:Cross-references: UNIPROT:Q06556; UNIPARC:UPI00000B92C0; EMBL:Z22150; NID:9288966; PI
 Best Local Similarity 42.3%; Pred. No. 1.5e-80;
 Matches 487; Conservative 184; Mismatches 310; Indels 171; Gaps 28;

1 MTNCKYKRLKSLGVGVSTGMLAPTVLQVVSASTSTSTSTASAGVGTSGTASSTGS 60
 1 MTNCKYKRLKSLGVGVSTGMLAPTVLQVVSASTSTSTSTASAGVGTSGTASSTGS 36
 61 GAATTAATTTATTCGPGSTPAVNAETPOQAQIPVAAATSSASSSSDG----- 113
 37 -ASVTTESPAIQTEBDQSGAEALIEPTTPAPQPSVSAVPEAAAMDEKIAEAPAH 95
 114 -KAPQ--VTSSTSPSTPAASNS-----GNOEASAEETEPQMEVEKYTVKEN 160
 96 EPAPKASVQAEASPPKAEATNTGQPTNTEQARSRSKAAEIAQTIEVEKLEVDKEN 155
 161 SKNIDKQKTPKSSSVNNKEDTKLIRNBDKLDLDVDTYRTYKTNEDGTIDVTVYKPK 220
 156 SSLTVMDG-----EKDKQKILKRDGNGRDIPIISRDKVKNQDGTMDVTLTVKPK 204
 221 QIDEGADVMA LDVSKKMSDDPFNNANKIKGLVLTLSKASNSDNDKHKYNSRNSVRL 280
 205 QIDEGADVMA LDVSKKMSDDPFNNANKIKGLVLTLSKASNSDNDKHKYNSRNSVRL 263
 281 MTTPRAISNIDISGTEBOLDKLDLDRKAKAND-NGVDLOGAHKAEIRNKEKKEK 339
 264 IDPFRKGSSTJDSMDAKKIDKELNEMVKAADINDGNGVDLOGAHKAEIRNKEKKEK 323
 340 KFGKRRHIVLFSSQSESTSYELQNSVREDTKLSTLSGAVTSSNPLPMPPIFNTHKNI 399
 324 RSGKRGIVLFSQSESTSYELQNSVREDTKLSTLSGAVTSSNPLPMPPIFNTHKNI 380
 400 DMLDDVKNLVKLGOTLGIAGLDNOSTLSLSTGSSLAGAFGGSLTEYTLTKKYSGD 459
 381 NVVDAKGLIDPFLKGLISQFNGAVDVAATVAGTLLGLGSPFLKAPLDTLSLADLTSK 440
 460 LKNOPTYTKRVGEGHPSERKKTGEIRPKSEIEPKIKELFENNNKNDKSWTEWIF 519
 441 INSEKPYSRVSGVYKRSYFDR-EVDKVGPKILVKKK--GNLKKRQPKOTDTRL- 495
 520 DKLSTETKIRKQKQETLMKLELYLTKKRYHYNNHLSAIAKAAQOEGTFYVVDV 579
 496 SSLGNSLTKKIKQDMMDKLDNLNFRQYQFVNNHLSAIAKAAQOEGTFYVVDV 555
 580 LKTSKRVKQVES-----TEDKKKEDREDIEKRNKFPNNTLKQSEGGKDPFEDVDKA 635
 556 PERIAKEINSQVSEAYTNHKKAEAREBEAKGRNEKFDYTLKEMSESQK-FEKDVEDP 614
 636 EKPQDILNNVYTFEFEDGVNVKNQNSQVSSNNNSLHNSYKVTAKASDASWMSLY- 693
 615 EKPQDILNNVYTFEFEDGVNVKNQNSQVSSNNNSLHNSYKVTAKASDASWMSLY- 664
 694 --SNKSLETLTSSKQK-----NSBQKSKNKEVYKKAASNSLSPLSP 750
 665 SSTMSSTLWLSKDKALQSGETLTLKYLKTHDKFLAPQTRSKRSIDTSENKKS 724
 751 VTKDIISNTVANKINQEVKANKLDVGLTYTKEFVVPVVEGSEV--PIPEKPLVEMTPLY 810
 725 VTEKVIYTSQVKKINDKVKKEKLDVSLVSKETVRKQVEPNV--PDVTEQEKELPDL 781
 811 VYAINNYP-----TPDIP-----TPQLPREDLEISGHPGVVDIYEDTGTABG-- 855
 782 ADSEBSQSPSTPPLPSPSPVSTPSTBGPREGNNL-GGQSBRTITEDSQSGNSGN 840
 856 ---GAQNGVVSQENRDPV-----DITEDTOPGMSGNDATVVEEDTAPKRPDVLV 904
 841 PDSGNETVVEDTQTSQEDVGLGAPQGVIDFTEDSQPGMSGNSHITEDSKPSQEDVVI 900
 905 GGQSPDITEDTOPSVGSGN--DATVVEEDTAPK-- 937

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 6, 2006, 01:31:29 ; Search time 48 Seconds
(without alignments)
2096.724 Million cell updates/sec

Title: US-10-771-931-1

Perfect score: 5357
Sequence: 1 MTNCKYLRKLKSLVGLSVGT.....PTIIGAGLLSKRRDTEGN 1046

Scoring table: BIOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 80:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3346.5	62.5	1025	2	6S69790 fibronectin-binding
2	2138.5	39.9	1091	2	S33850 fibronectin-binding
3	409.5	7.6	659	2	S40043 adhesin - Streptoc
4	394	7.4	638	2	S54418 fibronectin-binding
5	354	6.6	961	2	G90053 hypothetical prote
6	351.5	6.6	1018	2	A32192 fibronectin-binding
7	339	6.3	1038	2	H90053 hypothetical prote
8	338.5	6.3	940	2	S19702 fibronectin-binding
9	325.5	6.1	1039	2	T30856 protein P2 - Strept
10	306	5.7	1117	2	S33851 fibronectin-binding
11	302	5.6	1164	1	PCSOAG IGA FC receptor pr
12	289	5.4	1134	2	A60234 fibronectin-binding
13	282	5.3	1092	2	S42798 fibronectin-binding
14	268.5	5.0	1875	2	S38173 myosin-like protei
15	263.5	4.9	1726	1	SA2QCM major merzozite su
16	263.5	4.9	1726	1	A45948 major merzozite su
17	263	4.9	2139	2	T18296 myosin heavy chain
18	257.5	4.8	2481	2	D90011 Pmb protein (limpo
19	248.5	4.6	2722	2	T20532 hypothetical prote
20	248	4.6	2663	1	S28261 centromere protein
21	247	4.6	1526	2	A45605 mature-parasite-in
22	245	4.6	1086	2	S16752 major merzozite su
23	241.5	4.5	853	2	T51505 hypothetical prote
24	241	4.5	2269	2	T28677 rhoptry protein -
25	240.5	4.5	1306	2	S22624 aggregation protei
26	240	4.5	1127	2	T28317 ORP MSV156 hypoch
27	239.5	4.5	1125	2	B90598 hypothetical prote
28	239.5	4.5	1125	2	B90598 membrane nucleas
29	239.5	4.5	2508	2	S61441 surface-associated

30	239.5	4.5	2738	2	E88320 protein F07A11.6 [
31	238.5	4.5	1163	2	G97236 ATPase involved in
32	237	4.4	1192	2	A71623 probable secreted
33	237	4.4	1296	1	HMS01F aggregation protei
34	236.5	4.4	1166	2	T28680 fibronogen-binding
35	236.5	4.4	3468	2	T34418 hypothetical prote
36	236.5	4.4	2523	1	T18477 hypothetical prote
37	235	4.4	1361	1	S45781 probable calcium-b
38	235	4.4	1832	2	S33441 EF protein - Strept
39	234	4.4	2401	2	T28676 rhoptry protein -
40	233.5	4.4	816	2	S64439 hypothetical prote
41	232.5	4.3	7160	2	T27935 hypothetical prote
42	231.5	4.3	1690	2	T13030 microtubule bindin
43	231	4.3	1256	1	A43829 nuclease-release
44	231	4.3	1473	2	A35186 salivary agglutini
45	230.5	4.3	1701	2	A26868 major merzozite su

ALIGNMENTS

RESULT 1

6S69790
fibronectin-binding protein II precursor - Streptococcus pyogenes
C/Species: Streptococcus pyogenes
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S69790, S72666
R/Kelkemyer, B. J. Talay, S. R. Chhatwal, G. S.
Mol. Microbiol. 17, 137-145, 1995
A/Title: Characterization of a novel fibronectin-binding surface protein in group A str
A/Reference number: S69790, MUID:96020668, PMID:7476200
A/Accession: S69790
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-1025 <RR>
A/Cross-references: UNIPROT:P72532, UNIPARC:UP1000017AC7A, EMBL:X83303, NID:G1070387, I
A/Experimental source: strain A75
A/Note: the authors translated the initiation codon TTG for residue 1 as Leu
R/Kelkemyer, B.
submitted to the EMBL Data Library, December 1994
A/Accession: S72666
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A/Cross-references: UNIPARC:UP100000AP5EB, EMBL:X83303, NID:G1070387, PIDN:CA58282.1;
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A/Gene: sfbII
C/Keywords: fibronectin binding; membrane bound
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-1025/Product: fibronectin binding
F/848-868/Region: fibronectin binding
F/869-907/Region: fibronectin binding
F/908-946/Region: fibronectin binding
F/999-994/Region: membrane anchor cleavage motif
F/999-1016/Domain: transmembrane #status predicted <TM>

Query Match 62.5% Score 3346.5; DB 2; Length 1025;

Best Local Similarity 64.0% Pred. No. 3.1e-130;
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QY	53	TAASSETSGAAVTTATTTATTTNGPOSTPAVAEATPOQAOTAPVAAA--TSTSSASS 110
DB	61	TAAS-GASGA-----TVAATNGPGSAPATSEATPOQAQAAPASAPTTVTSSSSSD 113
QY	111	SDGAPQAVTSSISPSPTAAASNGSNGSASATPEPTMEVEKTYTDKSKNTDKGKT 170
DB	114	SDAKTPRA-ASTTSSSTATVSPSNGSKNANAPQMDVBOYKXDKENSSITVAD--- 169

171 PRTGSSVNNKEDTKLIRNRDGLDIVDTRTVKTNEBDITDVTVKPKQIDEGADVMA 230
 170 -----KAKQKLRDRDNPDKDLPVKREKVNKGSTLDVTLKMPKQIDEGADVMA 221
 221 LLDVSKNSBEDPNNKKNKIKLVYTLTSKSNSSNDNDHKNNSSNSVLMFYREISNP 290
 222 LLDVSGQNTKKNKPKDRAKQIKKQVTLTGEPIDGKEN-----HNRNSVLMFYRKVSDP 277
 291 IDISGTEBQDLKLDLKKAKKANYDKGVDLQGAHKAKEIPNKEKKEKPKRHLYLF 350
 278 IEL---TTKQVDAKKEKRVDAKQMDGVDLQGAHKAKEIPKQKSKK---KQHLYLF 332
 351 SGGSTSFYELONSVRBDTKLSRLSGAVTSNPILPWPPIFNTHKNIIMLDVKNLYK 410
 333 SGGSTSFYDINK--SDSKILKTRVNMETTSNPLPPLPIFNTHKADMDVKKLIK 391
 411 LGQTLGIALDNIQSTLSLSTGSSLAGAFSGGSLTEYLTLKRYSGDLKENQDVTYK 470
 392 WGRKLGIBGLNDLMDTLKLAGAASGVGGFAGGSLTEYLSLKEVQSDRLNLSQFYERK 451
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 507 ABEALAKVDYFPRYDYIYNNLSALAEAKMAOQEGITPYSVDVTLKTSKRYKQ 566
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 685 QAEKBEKPLTYTKKANDKQKRETLKQOESRIRIKRAASSEBNTVETIISNLSYK 744
 764 INN-QEYKGNKLDVLYTKETVPVVDGVRV--PIPEKPLVEBMTPLYPALPNYPP 820
 745 INNGKDTNNKLEBVMYSYKPMPIPELIDIVVVPQVPEKPLVEBMTPLYPALPNY 801
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 980 QAVYTKAAHMLPASGDRKASPTTAFTITGAAGLISKKRRDREN 1025

RESULT 2
 533850
 fibronectin-binding protein - Streptococcus dysgalactiae
 C/Species: Streptococcus dysgalactiae
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S33850, S32632
 R.J. Lindgren, P.E.; McGavin, M.J.; Signaes, C.; Gues, B.; Gurnaidappa, S.; Hoeoek, M.; Li
 Bui, J.; Blochm, 214, 819-827, 1993
 Article: Two different genes coding for fibronectin-binding proteins from Streptococcus
 #Reference number: S33850, M01D:93307299, PMID:831691

A: Molecule type: DNA
 A: Residues: 1-1091 <LIN>
 A: Cross-references: UNIPROT:Q06556, UNIPARC:UPI00000892C0, EMBL:Z22150, NID:G288968, PI
 Query Match 39.9%; Score 2138.5; DB 2; Length 1091;
 Best Local Similarity 42.3%; Pred. No. 1.5e-80;
 Matches 487, Conservative 184, Mismatches 310, Indels 171, Gaps 28;

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 61 GAAVTAATTAATTAATNGGPOSTPAVAEATPOFOAIPAAATSTSSASSSDG----- 113
 37 -ASVTTESPAIQTEDDQSGAALAEPTPAQTPSPSTVASVAPAAAMADKKGIAEAPAH 95
 114 -KAPQ--VTSSTPSTPAASSN-----GSHQBSAELEPOTMEKXTVDKEN 160
 96 BPAPKQVQABAPAPAGAEATVTGQPTTEQARSRSKRAEALPOTTEVEKLEVDKEN 155
 161 SKLNIKQDKTPTGSSVNNKEDTKLIRNRDGLDIVDTRTVKTNEBDITDVTVKPK 220
 156 SSLTYKQD-----EKDKLIKGRDNGQDIPDISHDVAVNGDGTMDVTLTYKPK 204
 221 QIDEGADVALLDVSKNSBEDPNNKKNKIKLVYTLTSKSNSSNDNDHKNNSSNSVRL 280
 205 QIDEGADVALLDVSKNSBEDPNNKKNKIKLVYTLTSKSNSSNDNDHKNNSSNSVRL 263
 261 MTFREISNPIDISGTEBQDLKLDLKKAKKANYD--WGVDLQGAHKAKEIPNKEK 339
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 441 INSEKFDYSRRGSEKYNRSYFDR--EVDKVGKPLVEKIL---GNLKKPQKQDVTM 495
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 751 VTMDIISNTVANKLNQOEVKANKLDVLYTKETVPVVDGVRV--PIPEKPLVEBMTPL 810
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 905 GQGSNTEVVDQTSQEDIVLGPGQVDFTEDSQCGMSGNSSHTTEDSKPSQEDVILI 937

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om protein - protein search, using sw model

Run on: JULY 6, 2006, 01:28:04 ; Search time 316 Seconds

3061.919 Million cell updates/sec

US-10-771-931-1
Perfect Score: 5357

sequence: 1 MINCKYKLRKLSVGLYSVT.....PTTGAAGLSKKRDTBGN 1046

Scoring Table:	BLOSUM62	Garnot	Garnot
10	0	0	0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Database : UniProt_7.2:*
1: uniprot_prot.*
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2: uniprot_crembl:

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5357	100.0	1046	2	084941_STRPY	084941 streptococc
2	3575.5	60.7	1027	2	093751_STRPY	093751 streptococc
3	3501	65.4	1026	2	048R34_STRPM	048R34 streptococc
4	3412.5	63.7	1023	2	093753_STRPY	093753 streptococc
5	3371.5	62.9	1025	2	054507_STRPY	054507 streptococc
6	3370	62.9	1026	2	09X336_STRPY	09X336 streptococc
7	3357.5	62.7	1025	2	P72552_STRPY	P72552 streptococc
8	3164.5	59.1	1013	2	09L950_STRPY	09L953 streptococc
9	3132.5	58.5	1015	2	093750_STRPY	093750 streptococc
10	2973.5	55.5	1013	2	093752_STRPY	093752 streptococc
11	2878.5	53.7	954	2	06YB06_STRPY	06Yb06 streptococc
12	2834	52.9	1022	2	093754_STRPY	093754 streptococc
13	2779.5	51.9	963	2	093749_STRPY	093749 streptococc
14	2654.5	49.6	1029	2	09X292_STRPY	09X292 streptococc
15	2571	48.0	862	2	09RPF8_STRPY	09RPF8 streptococc
16	2531	47.2	923	2	09S372_STRPY	09S372 streptococc
17	2488	46.4	865	2	09S4U9_STRPY	09S4U9 streptococc
18	2465	46.0	873	2	09S4K0_STRPY	09S4K0 streptococc
19	2460.5	45.9	872	2	09S4U3_STRPY	09S4U3 streptococc
20	2439.5	45.5	854	2	09S3P8_STRPY	09S4K0 streptococc
21	2329	43.5	881	2	09ARJ4_STRPY	09S3B8 streptococc
22	2138.5	39.9	1091	2	026S56_STRPY	09Rf14 streptococc
23	2102	39.2	746	2	08V995_STRPY	006556 streptococc
24	1458.5	27.0	409	2	09XBD9_STRPY	08V995 streptococc
25	1391.5	26.0	456	2	09XCK8_STRPY	09XBD9 streptococc
26	1388.5	25.9	471	2	09RZP8_STRPY	09XCK8 streptococc
27	1376.5	25.1	447	2	09R0R7_STRPY	09RZP8 streptococc
28	1343	25.1	452	2	09XCK2_STRPY	09R0R7 streptococc
29	1331.5	24.9	439	2	09R0R8_STRPY	09XCK2 streptococc
30	1276	23.8	454	2	09S4I8_STRPY	09XCK2 streptococc
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33	1247.5	23.1	435	2	09x9C0_STRPY	09x960_strptocccc
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35	1229	22.9	410	2	09PD03_STRPY	09dfld9_strptocccc
36	1219	22.8	253	2	09d49Z_STRPY	09d4d2_strptocccc
37	1191	22.2	434	2	09x6H2_STRPY	09x6H2_strptocccc
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40	1064	19.9	421	2	09xZP5_STRPY	09xzt5_strptocccc
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42	845.5	15.8	564	2	0300K5_STRSU	0300K5_strptocccc
43	806.5	15.1	261	2	09RFU5_STRPY	09rfU5_strptocccc
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45	708.5	13.2	250	2	09x6H0_STRPY	09x6H0_strptocccc

ALIGNMENTS

RESULT 1
084941

ID	084941_STRPY	PRELIMINARY;	PRT;	1046 AA
AC	084941:			

DI 01-NOV-1998, integrated into UniProtKB/TrEMBL.
 DI 01-NOV-1998, sequence version 1.

07-FEB-2006, entry version 25.
Serum opacity factor

Streptococcus pyogenes

Streptococcus.

RN [1]

RC STRAIN=T2MR;

RA Courtney H.S., Hasty D.L., Li Y., Chiang H.C., Thacker J.L.

"Serum opacity factor is a major fibronectin-binding protein and a

Mol. Microbiol. 32:89-98 (1999).

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Distributed under the Creative Commons Attribution license (<http://creativecommons.org/licenses/by/4.0/>)

----- CC -----
----- DB -----

BMET: AFO19890: AAC32E05 1 - 1 Comand's dwn

DR GO: GO:0009986; c:cell surface; IEA.
DR GO: GO:0009275; c:cell wall (sensu Gram-negative Bacteria); IEA.

DR GO: 0007155: P:cell adhesion: TRA
DA GO: 0016020; C:membrane; LKA.

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DR      InterPro: IPR005877: GPro YSTRK
DA      InterPro: IPR004231: Fibron_repeat_bd
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DR      interPro; IPR002035; VWF A.
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100	100

DR SMART; SM00327; VWA; 1.

DR PROSITE; PS50847; GRAM_POS_ANCHORI

SO SEQUENCE 1046 AA; 114914 MW; B12CF6B688059B62 CRC64;

Query Match	Score	DB 2;	Length
100.0%	5357;	DB 2;	1046;

Matches 1046; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 M T N C K Y K L R K L S V G L S V C T M L I A P T V L V Q E V S A S T T S T E T S T A S A G V G T S G T A S E T G S 6

1 MINCKIARKLSVGLSVGIMLIAPIVLVQBRVSASTTSTETSTASAGVGTSGTASSETGS 60

02 GMAVIAKIIIMINGFUSIPAVABAI PUPUAGIAPVAANAISISBASSSSBDGAPQAVT 12C


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Db 61 GAAVTTATTTATNGGPOSTPAVAEATPOPOAIAVPAATSTSSASSSSSGKAPAVT 120
Qy 121 SSTSPSTPAASAASNGNOEASAEETEPOTMEVEKTYVDKENSANI KQKPTKSSVNN 180
Db 121 SSTSPSTPAASAASNGNOEASAEETEPOTMEVEKTYVDKENSANI KQKPTKSSVNN 180
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Qy 241 DDPNNAOKTKI KQVKTITLSKASNSDDEKHTNRSNRYRLMTPTFRISINPIDI SKTBEQ 300
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Qy 481 SERKKTGEIPKSEIBPKIKELFENNKNQNDKSWTEWIPDKLSLTERIQAKOBTLMKL 540
Db 481 SERKKTGEIPKSEIBPKIKELFENNKNQNDKSWTEWIPDKLSLTERIQAKOBTLMKL 540
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Db 781 YTKETVPVPEGEVVPPEKPLVEBPWTPLYPALPNPTPTDIPPOLPKQBEDLISGGG 840
Qy 841 PSVDIVEDTGTAGAGGANGSVSTOENRBDIVDITEDTQMGSGSNDATVVEEDTAPKR 900
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Db 901 DUVVGOSQSDPIDITEDTQPSVSGSNDATVVEEDTVPKRPSPSLVGGSDPIDITEDTQPGM 960
Qy 961 SSGSNGATVVEEDTVPKRVFHDNEPQAEKPNQPSLSLPQAPVYKAAHLLPASGDKREA 1020
Db 961 SSGSNGATVVEEDTVPKRVFHDNEPQAEKPNQPSLSLPQAPVYKAAHLLPASGDKREA 1020
Qy 1021 SFTIAPPTIIGAAGLSKKRRDTEGN 1046
Db 1021 SFTIAPPTIIGAAGLSKKRRDTEGN 1046

```

RESULT 2
093751 STRPY
093751 STRPY PRELIMINARY; PRT; 1027 AA.
Integrated into UniProtKB/TrEMBL.

```

DT 07-FEB-2006, entry version 16.
DE Serum opacity factor VT21.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21642587; PubMed=11782509;
RA Gillen C.M., Towse R.J., McMillan D.J., Delvecchio A.,
RA Stripakha K.S., Currie B., Kreikemeyer B., Chhatwal G.S.,
RA Walker M.J.
RT Immunological response mounted by Aboriginal Australians living in
RT the Northern Territory of Australia against Streptococcus pyogenes
RT serum opacity factor.
RL Microbiology 148:169-178(2002).
CC
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CC
EMBL: AB367014; AK52968.1; -, Genomic DNA.
DR GO; GO:0009986; C:cell surface; IEA.
DR GO; GO:0009275; C:cell wall (benu Gram-positive Bacteria); IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR004237; Pfam repeat_bd.
DR InterPro; IPR005877; Gpos YSIRK.
DR InterPro; IPR001899; Gram_YSIRK.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02986; Fm_bind; 3.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRfam; TIGR01168; YSIRK signal; 1.
DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
DR PROSITE; PS50234; VWF_A; 1.
SQ SEQUENCE 1027 AA; 112542 MW; 048239E8598A4C7A CRC64;

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Query Match 66.7%; Score 3575.5; DB 2; Length 1027;
Best local similarity 70.1%; Pred. No. 2.8e-134;
Matches 751; Conservative 98; Mismatches 153; Indels 69; Gaps 26;
Qy 1 MNCKYKRLKLSVGLSVGTMILAPTVLQVBSAST--TSTETSTASAGVSTGTAASE 57
Db 1 MNCKYKRLKLSVGLSVGTMILAPTVLQVBSASTTETSTPATTPSAGTGA----- 54
Qy 58 TSGGAATVATTTT-----ATNGGPOSTPAVAEATPOPOAIAVPAAT 102
Db 58 TSGGAATVATTTT-----ATNGGPOSTPAVAEATPOPOAIAVPAAT 102
Qy 103 STSSASSSSDGKAPQAVTSTSPSTPAASAASNGNOEASAEETEPOTMEVEKTYVDKENS 162
Db 103 STSSASSSSDGKAPQAVTSTSPSTPAASAASNGNOEASAEETEPOTMEVEKTYVDKENS 162
Qy 112 STSS--NSSSDGQIPK--TATSPSTPAASNN--SNQESAEETEPOTMEVEKTYVDKEN-Q 166
Db 112 STSS--NSSSDGQIPK--TATSPSTPAASNN--SNQESAEETEPOTMEVEKTYVDKEN-Q 166
Qy 163 LNIKQKTEKTSYVNNKQTKLIRNDRKLDIVDTKTVKTNBEGTIDVTYVVKQI 222
Db 163 LNIKQKTEKTSYVNNKQTKLIRNDRKLDIVDTKTVKTNBEGTIDVTYVVKQI 222
Qy 223 DEGADVMALLDVSKKMSSEDPNNAKNTKQVKTITLSKASNSDDEKHTNRSNRYRLMT 282
Db 223 DEGADVMALLDVSKKMSSEDPNNAKNTKQVKTITLSKASNSDDEKHTNRSNRYRLMT 282
Qy 283 FFRISINPIDI SKTBEQDLKLDLIRKKAKANVMGVLDGAIHKAREIPKKEKKRKG 342
Db 283 FFRISINPIDI SKTBEQDLKLDLIRKKAKANVMGVLDGAIHKAREIPKKEKKRKG 342
Qy 340 KRQHVLSQGSSTSYEIKN---KDDKRLQKTLTFTVTSNPPLPMPPIFNHTHKNIDML 402
Db 340 KRQHVLSQGSSTSYEIKN---KDDKRLQKTLTFTVTSNPPLPMPPIFNHTHKNIDML 402
Qy 403 DPKNLVKGOTLAGLADNOSTLSLSTGSLAGATLGGSLTEYLITAKYSGDLKE 462
Db 403 DPKNLVKGOTLAGLADNOSTLSLSTGSLAGATLGGSLTEYLITAKYSGDLKE 462
Qy 397 DDKILIKGRLGIBGLSKDKLSLSTGSLAGLGGSLTEYLITAKYSGDSLSKA 456
Db 397 DDKILIKGRLGIBGLSKDKLSLSTGSLAGLGGSLTEYLITAKYSGDSLSKA 456

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